547062

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
10 September 2004 (10.09.2004)

PCT

(10) International Publication Number
WO 2004/076692 A1

(51) International Patent Classification[7]: C12Q 1/68

(21) International Application Number:
PCT/GB2004/000770

(22) International Filing Date: 26 February 2004 (26.02.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
0304371.8 26 February 2003 (26.02.2003) GB

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— *of inventorship (Rule 4.17(iv)) for US only*

Published:
— *with international search report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2004/076692 A1

(54) Title: DNA SEQUENCE ANALYSIS

(57) Abstract: There is disclosed a method for determining the identity of one or more mutations or single nucleotide polymorphisms (SNPs) in a genome, comprising: a. contacting a sample genome, under conditions which permit template dependant oligonucleotide ligation, with a plurality of different oligonucleotide molecules which comprise (i) a first set of oligonucleotides each comprising a sequence of nucleotides that is complementary to a region on said genome that includes a known SNP site and which oligonucleotides are complementary to said region other than at a base at or near the 5' end of said oligonucleotides that is to be tested for complementarity to a base at the SNP site, each of said oligonucleotides comprising a unique label to identify both the base to be tested and the position of the SNP to be scored, (ii) a second set of oligonucleotides each comprising a sequence of nucleotides complementary to a region on said target genome for hybridisation with said target genome adjacent the 5' end of an oligonucleotide of said first oligonucleotide set, and a surface capture moiety, a phosphate moiety being located at any of either the 5' end of said first set of oligonucleotides or the 3' end of said second set of oligonucleotides, any resulting ligated oligonucleotide being immobilised on a solid support via the surface capture moiety, b. analysing said solid support for the identity of one or more of said unique labels and comparing the defined bases in any of said immobilised oligonucleotides to those of the reference one or more SNPs.